

FIGURE 1

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1 AAGTGTAAAGCCTCCGAGGCCAAGGCCCTGCTACTGCCGCGCTGCTTCTAGTGGCGGTTCCGCCCTGGGTGTACCCGCGCCGCGCGAGGA 100
101 AGCCACTGCAACAGGACCGGAGTGGAGCGCGCGCAGCATGAAGCGCGCAGGCCCGCTCCATAGCGCACGTGGGACGGTCCGGGCGCGCGCGGGA 200
201 AGGAAAATGCACATGGCAGCAGCAATGGAAACAGAACAGCTGGGTGTGAGATATTGAAACTCGGGACTGTGAGGAGAAATTGAAATCAGAGGATCGG 300
M A A A M E T E Q L G V E I F E T A D C E E N I E S Q D R 29
301 CCTAAATTGGAGCCTTTTATGTTGAGCGGTATTCTGAGTCACTTAAAGCTGCTTGGCGATACCAGAAAATATCATGGCTACATGATGGTAAAG 400
30 P K L E P F Y V E R Y S W S Q L K K L L A D T R K Y H G Y M H A K A 63
401 CACCACATGATTTCATGTTTGTGAAGAGGAATGATCCAGATGGACCTCATTCAGACAGAACTATTACCTTGGCATGTCTGGTGAACAGAGAAAATAC 500
63 P H D F M F V K R N D P D G P H S D R I Y Y L A M S G E N R E N T 96
501 ACTGTTTTATTTCGAAATCCCAAACTATCAATAGAGCAGCAGTCTTAATGCTCTCTTGGAGGCTCTTTTGGATCTTTTTCAGGCAACACTGGACTAT 600
96 L F Y S E I P K T I N R A A V L H L S W K P L L D L F O A T L D Y 129
601 GGAATGTATTCTCGAGAAGAAGAACTATTAGAGAAAGAAACCGATTCGAAACAGTGGAAATGCTTCTTACGATTATCACCAGGAAGTGAACATTTT 700
130 G H Y S R E E E L R E R K R I G T V G I A S Y D Y H Q G S G T F L 163
701 TGTTCAGGCGGCTAGTGGATTTATCAGTGAAGAGTGAAGGAGTTACGCAAGAACTTTAAGGCCAACTTAGTGGAACTAGTTGTGTC 800
163 F Q A G S G I Y H V K A D G G G P Q G F T Q Q P L R P N L V E T S C P 196
801 CAACATACGGATGGATCCAAAATTATGCCCGCTGATCCAGACTGGATGCTTTTATACATAGCAAGATATTGGATATCAACATGTAACAGAGAA 900
196 N I R M D P K L C P A D P D M I A F I H S N D I W I S N I V T R E 229
901 GAAAGGAGACTCACTTATGTGCACAAAGAGCTAGGCAACATGGAGAGATGCCAGATCAGCTGGAGTGGCTACCTTTGTTCTCCAGAGAAATTTGATA 1000
230 E R R L T Y V H N E L A N H E E D A R S A G V A T F V L Q E E F D R 263
1001 CATATTCTGGCTATTGCTGGTGTCCAAAAGCTGAAACAACCTCCAGTGGTGGTAAATCTTAGAATCTATATGAAGAAAATGATGAATCTGAGGTGGA 1100
263 Y S G Y W M C P K A E T T P S G G K I L R I L Y E E N D E S E V E 296
1101 AATTATTTCATGTACATCCCTATGTTGGAAACAGGAGGAGGAGTTCATTCGGTATTCCTAAACAGGTACAGCAATCCCTAAAGTCACTTTTAAGATG 1200
296 I I H V T S P M L E T R R A D S F R Y P K T G T A N P K Y T F K H 329
1201 TCAGAAATATGATTGATGCTGAAGGAAGGATCATAGATGCTATAGATAAGGAACATACTCAACCTTTTGAGATTCTATTGAAGGAGTGAATATATTG 1300
330 S E I M I D A E G R I I D V I D K E L I Q P F E I L F E G V E Y I A 363
1301 CCAGAGTGGATGGACTCCTGAGGGAATATGCTTGGTCCATCTCTACTAGATCGCTCCAGACTCGCTACAGATAGTGTGATCTCACTGAAATATT 1400
363 R A G M T P E G K Y A M S I L L S Q T R L Q I V L I S P E L F 396
1401 TATCCAGTAGAAGATGATGTTATGGAAGGAGAGACTCTTAGTCTAGTGGCTGATTCGTGAGGCCACTAATTTATATGAAGAAACACAGACATC 1500
396 I P V E D D V M E R Q R L I E S V P D S V T P L I I Y E E T T D I 429
1501 TGGATAAATATCCATGACATCTTTCAATGTTTTCGCCAAGTCAAGAGAGGAAATGAGTTTATTTTGGCTCTGAATGCAAAACAGGTTCCTGCTATT 1600
430 W I N I H D I F H V F P Q S H E E I E F I F A S E C K T G F L 463
1601 TATACAAATTTACATCTATTAAAGGAAGCAAAATATAAGGATCCAGTGGTGGCTGCTGCTCAAGTGATTTCAAGTGTCTATCAAGAGGAGAT 1700
463 Y K I T S I L K E S K Y K R S S G G L P A P S D F K C P I K E E I 496
1701 AGCAATTACCAGTGGTGAATGGGAGTTCTTGGCGCGCATGGATCTAATATCCAGTTGATGAAGTCAGAGGCTGGTATATTTGAAGGCACCAAGAC 1800
496 A I T S G E W E V L G R H G S N I Q V D E V R R L V Y F E G T K D 529
1801 TCCCTTTAGAGCATCACTGTACGTAGTCACTTACGTAATCTGGAGAGGTGACAAAGGCTGACTGACCTGGCTACTACATCTTCTGCTGATCAGTC 1900
530 S P L E H H L Y V V S Y V N P G E V T R L T D R G Y S H S C C I S Q 563
1901 AGCACTGTGACTTCTTTAAGTAAGTATAGTAACAGAGAAATCCACACTGTGTGCTCTTTACAAGCTATCAAGTCTGAGATGACCACTTCCAA 2000
563 H C D F F I S K Y S N Q K N P H C V S L Y K L S S P E D D P T C K 596
2001 AACAAAGAAATTTGGGCCACCAATTTGGATTCAAGAGGCTCTCTCTGACTATCTCTCCAGAAATTTCTCTTTGAAAGTACTACTGGATTACA 2100
596 T F E G A T I L D S A G P L P D Y T P P E I F S F E S T T G F T 629
2101 TTGTATGGGATGCTCTACAGCTCATGATCTACAGCTGGAAAGAAATATCTACTGTGCTTTCATATATGTTGGTCTCAAGTGGAGTGGTGAATA 2200
630 L Y G M L Y K P H D L Q P G K K Y P T V L F I Y G G P Q V Q L V M N 663
2201 ATCGGTTAAAGGAGTCAAGTATTTCCGCTGAAATACCTTAGCCTCTCTAGGTTATGTTGTTGATGATAGACAAACAGGATCTCTCAACAGGAGT 2300
663 R P K G V K Y F R L M T L A S L G Y V V V I D N R G S C H R G L 696
2301 TAAATTTGAAGCGGCTTTAAATATAAAATGGGTCAAATAGAAATGACGATCAGGTGGAAGGACTCCAAATATCTAGCTTCTGATATGATTTTCATGAC 2400
696 K F E G A F K Y K M G Q I E I D D Q V E G L O Y L A S R Y D F I D 729
2401 TTAGATCGTGTGGGCAATCCAGGCTGGTCTATGAGGATACCTCTCCCTGATGGCATTAAAGCAGAGTCAAGATATCTCAGGTTGCTATTCTGGGG 2500
730 L D R V G I H G Y L S L K A L N Q R S D I F R V A I A G A 763
2501 CCCCCTCACTCTGATCTTCTATGATACAGGATACAGGAGCTTATATGAGTCAACCTGACAGAGTGAACAGGCTTACTTAGGATCTGTGGC 2600
763 P V T L W I F Y D T G Y T E R Y N G H P D Q N E Q G Y Y L G S V A 796
2601 CATGCAAGCAGAAAGTTCCCTCTGAACCAATGTTTACTGCTCTTACATGTTTCTGATGAGAAATGCCATTTTCACATACCACTATATTACTG 2700
796 H Q A E K F P S E P N R L L L L N G F L E N V H F A H T S I L L 829
2701 AGTTTTTGTAGGAGGCTGGAAAGCCATATGATTTCAGATCTATCTCAGGAGAGACAGCATAGAGTTCTGATCGGAGAACATTATGAACCTG 2800
830 S F L V R A G K F P Y D L Q I Y P O A G S I R V P E S G E Y E L H 863
2801 ATCTTTTGCACCTACCTCAAGAAACCTTGGATCAGTATGCTGCTTAAAGTGATATAATTTGACCTGTGTAGAACTCTCTGATATACACCTGGTA 2900
863 L L H Y L Q E N L G S R I A A L K V I 882
2901 TTTAACCAATGAGGAGGTTAATCAACAGAAACACAGATGATCATCATTTTGATACCTGCCATGTACATCTACTCTGAAATAAATGTGGT 3000
3001 CCATCAGGGGCTACGGTTTGTGGTAGTAACTAATACCTTAACCCACATGCTCAAAATCAATGATACATATCTCTGAGAGACCCAGCAATACCATA 3100
3101 AGAATTACTAAAAA 3127

FIGURE 2

SUBSTITUTE SHEET (RULE 26) RO/AU

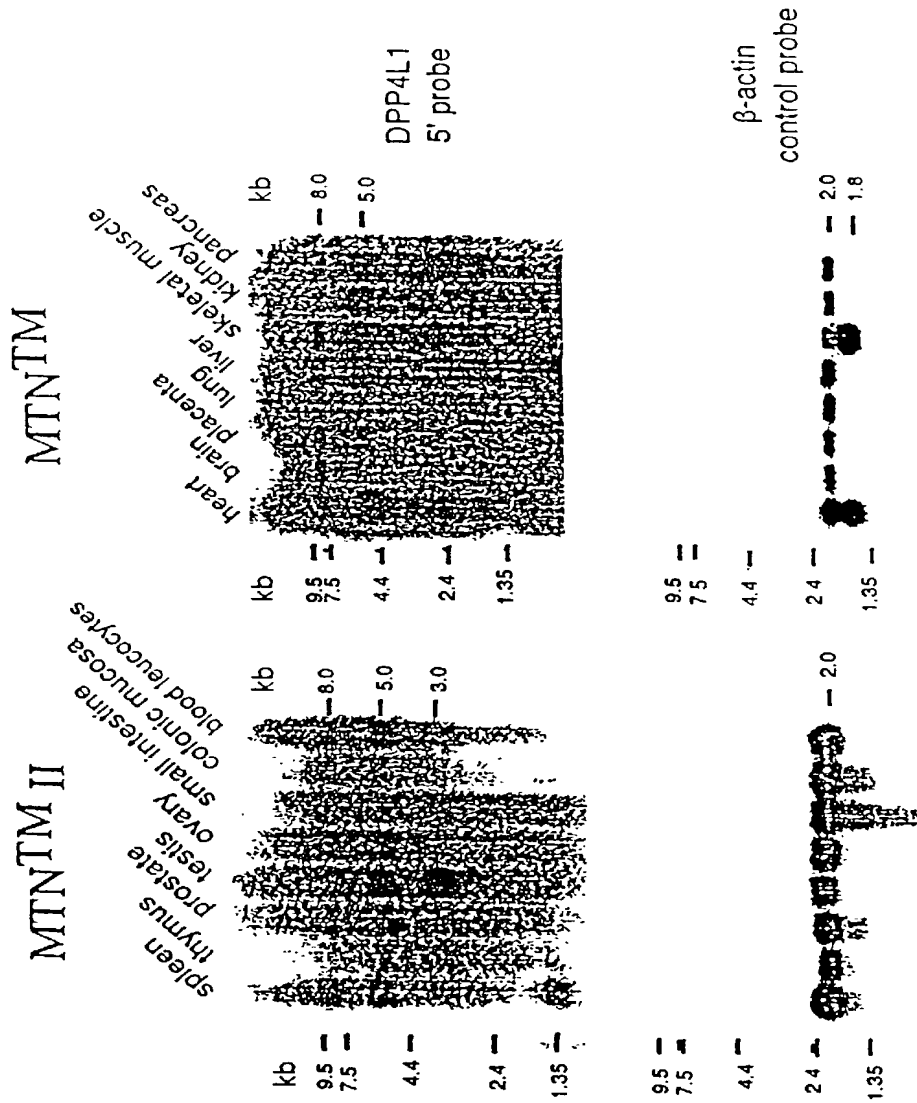


FIGURE 4

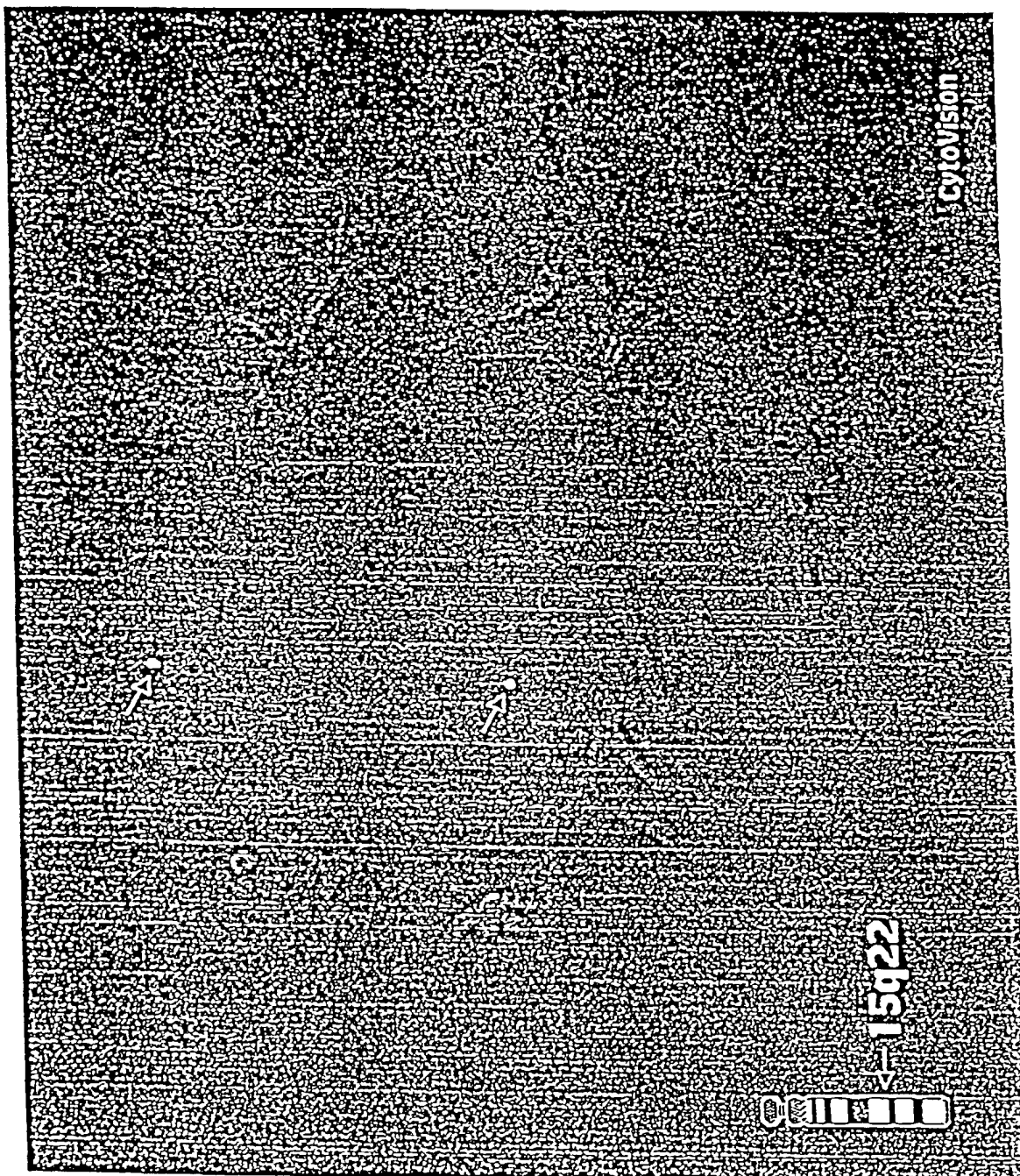


FIGURE 5

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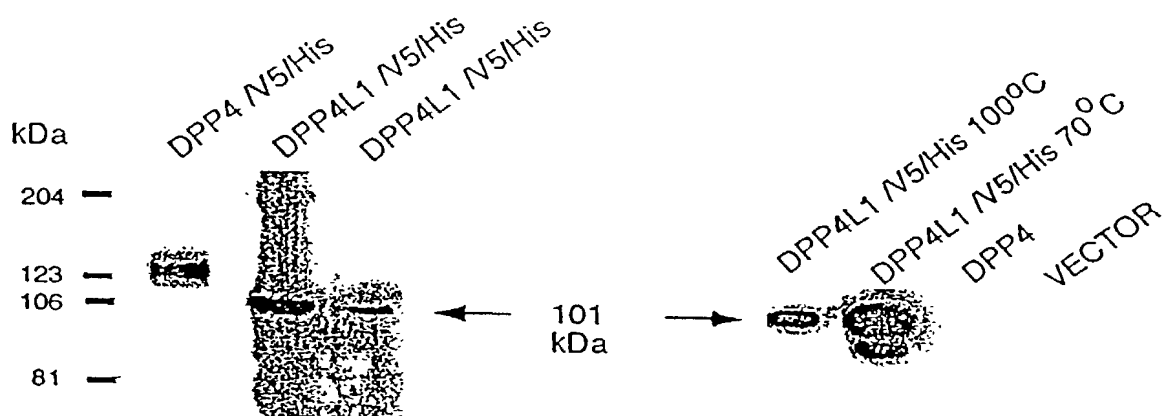


FIGURE 6

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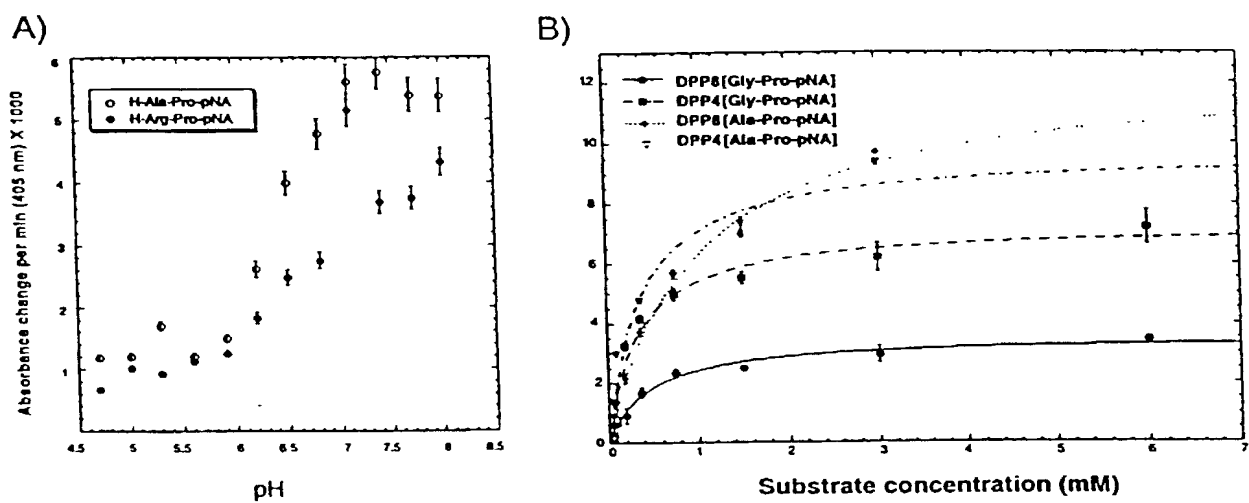


FIGURE 7

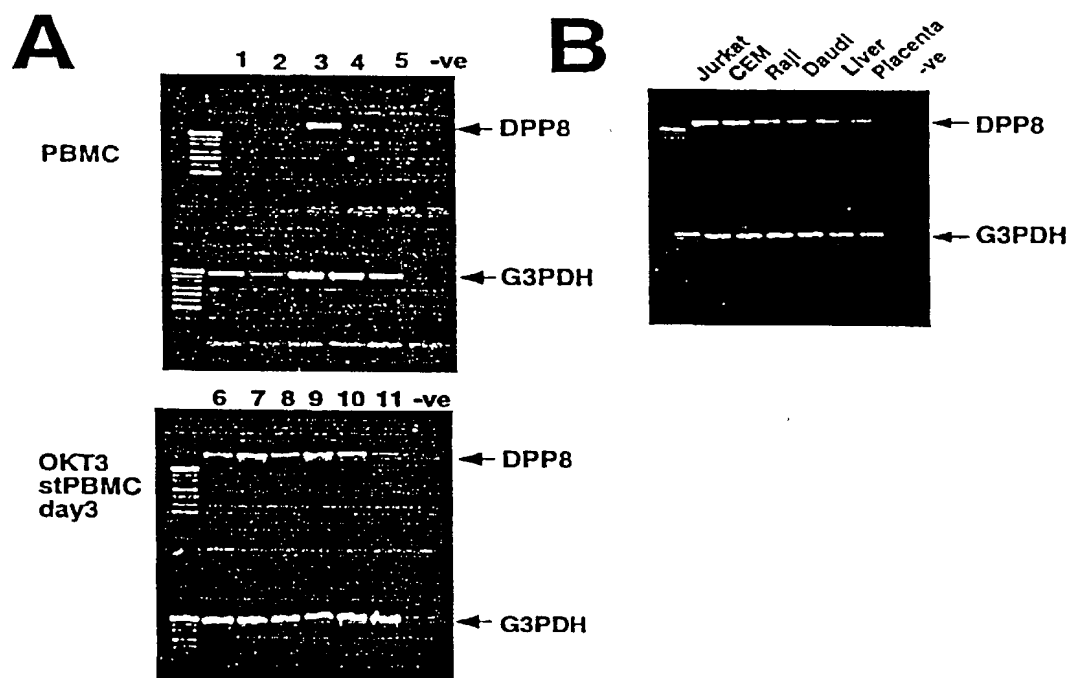


FIGURE 8

FIGURE 9A

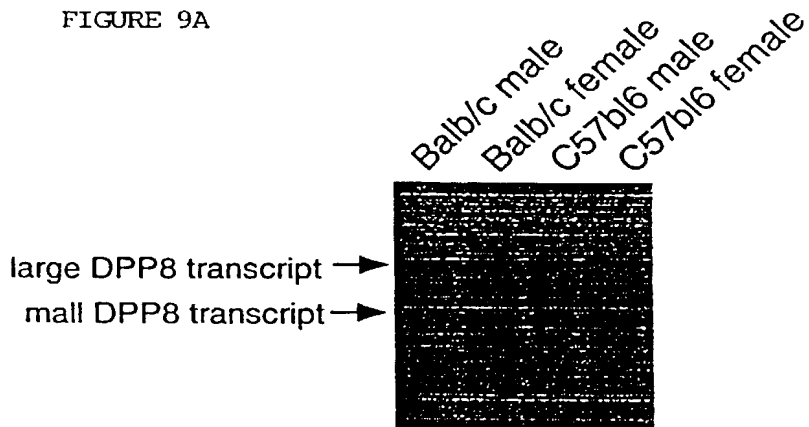


FIGURE 9B

